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RAW SEQUENCE LISTING   DATE: 12/22/2000
PATENT APPLICATION: US/09/486,167A   TIME: 10:54:34

Input Set : A:\ES.txt
Output Set: N:\CRF3\12222000\I486167A.raw

```
 5 <110> APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN
 7         UNIVERSITE DE MONS-HAINAUT
11 <120> TITLE OF INVENTION: PEROXISOME-ASSOCIATED PEPTIDE, NUCLEOTIDE SEQUENCE ENCODING SAID PEPTIDE
12         AND THEIR USES IN THE DIAGNOSTIC AND/OR THE TREATMENT OF LUNG INJURIES AND
13         DISEASES? AND OF OXIDATIVE STRESS-RELATED DISORDERS
17 <130> FILE REFERENCE: VANM143.001A
21 <140> CURRENT APPLICATION NUMBER: US 09/486,167A
23 <141> CURRENT FILING DATE: 2000-08-15
27 <160> NUMBER OF SEQ ID NOS: 4
31 <170> SOFTWARE: PatentIn version 3.0
35 <210> SEQ ID NO: 1
37 <211> LENGTH: 805
39 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapiens
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47 <221> NAME/KEY: CDS
49 <222> LOCATION: (193)..(681)
53 <400> SEQUENCE: 1
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56 ctgagacgct cagcgggcta tatactcgtc ggtggggccg gcggtcagtc tgcggcagcg     120
58 gcagcaagac ggtgcagtga aggagagtgg gcgtctggcg gggtccgcag tttcagcaga     180
60 gccgctgcag cc atg gcc cca atc aag gtg gga gat gcc atc cca gca gtg    231
61            Met Ala Pro Ile Lys Val Gly Asp Ala Ile Pro Ala Val
62             1               5                  10
64 gag gtg ttt gaa ggg gag cca ggg aac aag gtg aac ctg gca gag ctg      279
65 Glu Val Phe Glu Gly Glu Pro Gly Asn Lys Val Asn Leu Ala Glu Leu
66    15                  20                  25
68 ttc aag ggc aag aag ggt gtg ctg ttt gga gtt cct ggg gcc ttc acc      327
69 Phe Lys Gly Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe Thr
70 30                  35                  40                  45
72 cct gga tgt tcc aag aca cac ctg cca ggg ttt gtg gag cag gct gag      375
73 Pro Gly Cys Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala Glu
74             50                  55                  60
76 gct ctg aag gcc aag gga gtc cag gtg gtg gcc tgt ctg agt gtt aat      423
77 Ala Leu Lys Ala Lys Gly Val Gln Val Val Ala Cys Leu Ser Val Asn
78             65                  70                  75
80 gat gcc ttt gtg act ggc gag tgg ggc cga gcc cac aag gcg gaa ggc      471
81 Asp Ala Phe Val Thr Gly Glu Trp Gly Arg Ala His Lys Ala Glu Gly
82             80                  85                  90
84 aag gtt cgg ctc ctg gct gat ccc act ggg gcc ttt ggg aag gag aca      519
85 Lys Val Arg Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu Thr
86    95                  100                 105
88 gac tta tta cta gat gat tcg ctg gtg tcc atc ttt ggg aat cga cgt      567
89 Asp Leu Leu Leu Asp Asp Ser Leu Val Ser Ile Phe Gly Asn Arg Arg
90 110                 115                 120                 125
92 ctc aag agg ttc tcc atg gtg gta cag gat ggc ata gtg aag gcc ctg      615
93 Leu Lys Arg Phe Ser Met Val Val Gln Asp Gly Ile Val Lys Ala Leu
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94              130             135             140
96 aat gtg gaa cca gat ggc aca ggc ctc acc tgc agc ctg gca ccc aat          663
97 Asn Val Glu Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro Asn
98              145             150             155
100 atc atc tca cag ctc tga ggccctgggc cagattactt cctccacccc              711
101 Ile Ile Ser Gln Leu
102             160
104 tccctatctc acctgcccag ccctgtgctg gggccctgca attggaatgt tggccagatt      771
106 tctgcaataa acacttgtgg tttgcggaaa aaaa                                  805
109 <210> SEQ ID NO: 2
111 <211> LENGTH: 162
113 <212> TYPE: PRT
115 <213> ORGANISM: Homo sapiens
119 <400> SEQUENCE: 2
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122 1               5               10              15
125 Glu Gly Glu Pro Gly Asn Lys Val Asn Leu Ala Glu Leu Phe Lys Gly
126             20              25              30
129 Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe Thr Pro Gly Cys
130             35              40              45
133 Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala Glu Ala Leu Lys
134     50              55              60
137 Ala Lys Gly Val Gln Val Val Ala Cys Leu Ser Val Asn Asp Ala Phe
138 65              70              75              80
141 Val Thr Gly Glu Trp Gly Arg Ala His Lys Ala Glu Gly Lys Val Arg
142             85              90              95
145 Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu Thr Asp Leu Leu
146             100             105             110
149 Leu Asp Asp Ser Leu Val Ser Ile Phe Gly Asn Arg Arg Leu Lys Arg
150     115             120             125
153 Phe Ser Met Val Val Gln Asp Gly Ile Val Lys Ala Leu Asn Val Glu
154     130             135             140
157 Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro Asn Ile Ile Ser
158 145             150             155             160
161 Gln Leu
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167 <211> LENGTH: 780
169 <212> TYPE: DNA
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179 <222> LOCATION: (136)..(624)
183 <220> FEATURE:
185 <221> NAME/KEY: Unsure
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189 <223> OTHER INFORMATION: purine
193 <220> FEATURE:
195 <221> NAME/KEY: Unsure
197 <222> LOCATION: (323)..(323)
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205 <221> NAME/KEY: Unsure
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216 gcaggcagag caggccggaa aggagcaggt tgggagtgtg gtggggcccg cagcttcagc       120
218 agtgccgcgg tgact atg gcc ccg atc aag gtg gga gac acc att ccc tca        171
219               Met Ala Pro Ile Lys Val Gly Asp Thr Ile Pro Ser
220                1                 5                  10
222             gtg gag gta ttt gra ggg gaa cct gga aag aag gtg aac ttg gca gag      219
W--> 223        Val Glu Val Phe Xaa Gly Glu Pro Gly Lys Lys Val Asn Leu Ala Glu
224                 15              20              25
226             ctg ttc aag gac aag aaa ggt gtt ttg ttt gga gtc cct ggg gca ttt      267
227             Leu Phe Lys Asp Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe
228                 30              35              40
230             aca cct ggc tgt tcc aag acc cat ctg cct ggg ttt gtg gag caa gcc      315
231             Thr Pro Gly Cys Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala
232             45              50              55              60
234             gga gct cyg aag gcc aag gga gca caa gtg gtg gcc tgt ctg agt gtt      363
W--> 235        Gly Ala Xaa Lys Ala Lys Gly Ala Gln Val Val Ala Cys Leu Ser Val
236                 65              70              75
238             aat gat gyc ttc gtg act gca gag tgg ggt cga gcc cac cag gca gaa      411
W--> 239        Asn Asp Xaa Phe Val Thr Ala Glu Trp Gly Arg Ala His Gln Ala Glu
240                 80              85              90
242             ggc aag gtt cag ctc ctg gct gac ccc act gga gct ttt gga aag gag      459
243             Gly Lys Val Gln Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu
244                 95              100             105
246             aca gat tta cta cta gat gat tct ttg gtg tct ctc ttt ggg aat cgt      507
247             Thr Asp Leu Leu Leu Asp Asp Ser Leu Val Ser Leu Phe Gly Asn Arg
248             110             115             120
250             cgg cta aaa agg ttc tcc atg gtg ata gac aag ggc gta gta aag gca      555
251             Arg Leu Lys Arg Phe Ser Met Val Ile Asp Lys Gly Val Val Lys Ala
252             125             130             135             140
254             ctg aac gtg gag ccg gat ggc aca ggc ctc acc tgc agc ctg gcc ccc      603
255             Leu Asn Val Glu Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro
256                 145             150             155
258             aac atc ctc tca caa ctc tga ggccctgacc agaatgtcct ctgactctcc        654
259             Asn Ile Leu Ser Gln Leu
260                     160
262 catctcctcc acccagctct gggccaaagg cccagtacct ccttacctga gggccactgg      714
264 aatggaacct tgacaatatt tctgcaataa acagtttaat ttgtgaaaaa aaaaaaaaaa      774
266 aaaaaa                                                               780
269 <210> SEQ ID NO: 4
271 <211> LENGTH: 162
273 <212> TYPE: PRT
275 <213> ORGANISM: Rattus rattus
279 <220> FEATURE:
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                    PATENT APPLICATION:  US/09/486,167A     TIME: 10:54:34

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     283 <222> LOCATION: 17
     285 <223> OTHER INFORMATION: Glu or Gly
     288 <220> FEATURE:
W--> 290 <221> NAME/KEY: Modified-site
     292 <222> LOCATION: 63
     294 <223> OTHER INFORMATION: Leu or Pro
     297 <220> FEATURE:
W--> 299 <221> NAME/KEY: Modified-site
     301 <222> LOCATION: 79
     303 <223> OTHER INFORMATION: Ala or Val
     306 <400> SEQUENCE: 4
     308 Met Ala Pro Ile Lys Val Gly Asp Thr Ile Pro Ser Val Glu Val Phe
     309 1              5                  10                 15
W--> 312 Xaa Gly Glu Pro Gly Lys Lys Val Asn Leu Ala Glu Leu Phe Lys Asp
     313             20                  25                 30
     316 Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe Thr Pro Gly Cys
     317             35                  40                 45
W--> 320 Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala Gly Ala Xaa Lys
     321     50                  55                 60
W--> 324 Ala Lys Gly Ala Gln Val Val Ala Cys Leu Ser Val Asn Asp Xaa Phe
     325 65                  70                  75                 80
     328 Val Thr Ala Glu Trp Gly Arg Ala His Gln Ala Glu Gly Lys Val Gln
     329             85                  90                 95
     332 Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu Thr Asp Leu Leu
     333             100                 105                110
     336 Leu Asp Asp Ser Leu Val Ser Leu Phe Gly Asn Arg Arg Leu Lys Arg
     337             115                 120                125
     340 Phe Ser Met Val Ile Asp Lys Gly Val Val Lys Ala Leu Asn Val Glu
     341     130                 135                140
     344 Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro Asn Ile Leu Ser
     345 145                 150                 155                160
     348 Gln Leu
```

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Input Set : A:\ES.txt
Output Set: N:\CRF3\12222000\I486167A.raw

L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:281 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:290 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:299 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4